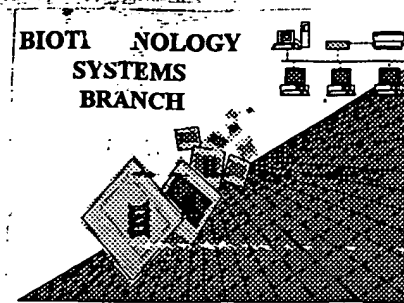


Dibrine

RAW SEQUENCE LISTING ERROR REPORT



#11

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/375,924A

Source: 1644

Date Processed by STIC: 11/30/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/375,924A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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1644

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/375,924A

DATE: 11/30/2000
 TIME: 11:13:28

Input Set : A:\abgx-2 cip.ST25.txt
 Output Set: N:\CRF3\11302000\I375924A.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Gallo, Michael
 4 Foord, Orit
 5 Junghans, Richard
 7 <120> TITLE OF INVENTION: GENERATION OF MODIFIED MOLECULES WITH INCREASED SERUM HALF-LIVES
 9 <130> FILE REFERENCE: ABGX-2 CIP
 11 <140> CURRENT APPLICATION NUMBER: US 09/375,924A
 12 <141> CURRENT FILING DATE: 1999-08-17
 14 <150> PRIOR APPLICATION NUMBER: US 60/096,868
 15 <151> PRIOR FILING DATE: 1998-08-17
 17 <160> NUMBER OF SEQ ID NOS: 10
 19 <170> SOFTWARE: PatentIn version 3.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 16
 23 <212> TYPE: PRT
 24 <213> ORGANISM: homo sapiens
 26 <400> SEQUENCE: 1
 28 Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr His Thr Cys Pro Pro
 29 1 5 10 15
 31 <210> SEQ ID NO: 2
 32 <211> LENGTH: 16
 33 <212> TYPE: PRT
 34 <213> ORGANISM: Artificial/Unknown
 36 <220> FEATURE:
 37 <221> NAME/KEY: misc_feature
 38 <222> LOCATION: ()..()
 39 <223> OTHER INFORMATION: modified
 42 <400> SEQUENCE: 2
 44 Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr His Thr Cys Pro Pro
 45 1 5 10 15
 47 <210> SEQ ID NO: 3
 48 <211> LENGTH: 12
 49 <212> TYPE: PRT
 50 <213> ORGANISM: Homo sapiens
 52 <400> SEQUENCE: 3
 54 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
 55 1 5 10
 57 <210> SEQ ID NO: 4
 58 <211> LENGTH: 12
 59 <212> TYPE: PRT
 60 <213> ORGANISM: Homo sapiens
 62 <400> SEQUENCE: 4
 64 Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
 65 1 5 10
 67 <210> SEQ ID NO: 5
 68 <211> LENGTH: 12
 69 <212> TYPE: DNA
 70 <213> ORGANISM: Homo sapiens

invalid Per 1.823 of new sequence rules,
 the <213> response is either
 Unknown, Artificial Sequence, or
 Scientific name

(Genus/species)
one of the three

Please give source
 of genetic material
 in <223> response
 (see circled portion
 of Item 12 on Enov
 summary sheet)

RAW SEQUENCE LISTING DATE: 11/30/2000
 PATENT APPLICATION: US/09/375,924A TIME: 11:13:28

Input Set : A:\abgx-2 cip.ST25.txt
 Output Set: N:\CRF3\11302000\I375924A.raw

```

72 <400> SEQUENCE: 5
73 tctctgggta aa
76 <210> SEQ ID NO: 6
77 <211> LENGTH: 12
78 <212> TYPE: DNA
79 <213> ORGANISM: Artificial/Unknown
81 <220> FEATURE:
82 <221> NAME/KEY: misc_feature
83 <222> LOCATION: ()..()
84 <223> OTHER INFORMATION: modified sequence
87 <400> SEQUENCE: 6
88 tccttaggga ag
91 <210> SEQ ID NO: 7
92 <211> LENGTH: 22
93 <212> TYPE: DNA
94 <213> ORGANISM: Artificial/Unknown
96 <220> FEATURE:
97 <221> NAME/KEY: misc_feature
98 <222> LOCATION: ()..()
99 <223> OTHER INFORMATION: primer 1
102 <400> SEQUENCE: 7
103 gggacccacg gggtagcagg gc
106 <210> SEQ ID NO: 8
107 <211> LENGTH: 36
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial/Unknown
111 <220> FEATURE:
112 <221> NAME/KEY: misc_feature
113 <222> LOCATION: ()..()
114 <223> OTHER INFORMATION: primer 2
117 <400> SEQUENCE: 8
118 cttccctaag gacatggaga ggcctctctg tgtgtg
121 <210> SEQ ID NO: 9
122 <211> LENGTH: 36
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial/Unknown
126 <220> FEATURE:
127 <221> NAME/KEY: misc_feature
128 <222> LOCATION: ()..()
129 <223> OTHER INFORMATION: primer 3
132 <400> SEQUENCE: 9
133 gattccttag ggaaggcaga gcccaaatct agtgac
136 <210> SEQ ID NO: 10
137 <211> LENGTH: 34
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial/Unknown
141 <220> FEATURE:
142 <221> NAME/KEY: misc_feature
143 <222> LOCATION: ()..()

```

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/375,924A

DATE: 11/30/2000
TIME: 11:13:28

Input Set : A:\abgx-2 cip.ST25.txt
Output Set: N:\CRF3\11302000\I375924A.raw

144 <223> OTHER INFORMATION: primer 4
147 <400> SEQUENCE: 10
148 gccggaattc ggtacgtgcc aagcatcctc gtgc

34

VERIFICATION SUMMARY

DATE: 11/30/2000

PATENT APPLICATION: US/09/375,924A

TIME: 11:13:29

Input Set : A:\abgx-2 cip.ST25.txt

Output Set: N:\CRF3\11302000\I375924A.raw

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